

SEQUENCE LISTING

<110> AYYOUB, Maha
VALMORI, Danila
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WAGNER, Claudia
STEVANOVIC, Stephan
PFREUNDSCHUH, Michael

<120> SSX-2 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES

<130> L0461.70158US00

<150> US 09/408,036

<151> 1999-09-29

<160> 51

<170> PatentIn version 3.2

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<213> Homo sapiens

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<222> (109)..(675)

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Met Asn Gly
1

gac gac gcc ttt gca agg aga ccc acg gtt ggt gct caa ata cca gag 165
Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln Ile Pro Glu
5 10 15

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Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe Ser Lys Glu
20 25 30 35

gag tgg gaa aag atg aaa gcc tcg gag aaa atc ttc tat gtg tat atg 261
Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met
40 45 50

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Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys Ala Thr Leu
55 60 65

cca cct ttc atg tgt aat aaa cgg gcc gaa gac ttc cag ggg aat gat 357
Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln Gly Asn Asp
70 75 80

ttg gat aat gac cct aac cgt ggg aat cag gtt gaa cgt cct cag atg 405
Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg Pro Gln Met
85 90 95

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Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys Pro Thr Thr	
135 140 145	
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Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly Glu His Ala	
150 155 160	
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Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile Tyr Glu Glu	
165 170 175	
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Ile Ser Asp Pro Glu Glu Asp Asp Glu	
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taatttcaga ttttttcttc tgcatttaca cacacacgca cacaaccac accacacaca	1115
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Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
 35 40 45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
 50 55 60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
 65 70 75 80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
 85 90 95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
 100 105 110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
 115 120 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
 130 135 140

Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
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Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile
 165 170 175

Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
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 Met Asn Gly
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 Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln Ile Pro Glu
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 aag atc caa aag gcc ttc gat gat att gcc aaa tac ttc tct aag gaa 213

Lys 20	Ile	Gln	Lys	Ala	Phe 25	Asp	Asp	Ile	Ala	Lys 30	Tyr	Phe	Ser	Lys	Glu 35	
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Pro	Pro	Phe 70	Met	Cys	Asn	Lys	Arg 75	Ala	Glu	Asp	Phe	Gln 80	Gly	Asn	Asp	
ttg gat aat gac cct aac cgt ggg aat cag gtt gaa cgt cct cag atg 405																
Leu	Asp	Asn	Asp	Pro	Asn	Arg 90	Gly	Asn	Gln	Val 95	Glu	Arg	Pro	Gln	Met	
act ttc ggc agg ctc cag gga atc tcc ccg aag atc atg ccc aag aag 453																
Thr	Phe	Gly	Arg	Leu	Gln 105	Gly	Ile	Ser	Pro 110	Lys	Ile	Met	Pro	Lys	Lys 115	
cca gca gag gaa gga aat gat tcg gag gaa gtg cca gaa gca tct ggc 501																
Pro	Ala	Glu	Glu	Gly 120	Asn	Asp	Ser	Glu 125	Glu	Val	Pro	Glu	Ala	Ser	Gly 130	
cca caa aat gat ggg aaa gag ctg tgc ccc ccg gga aaa cca act acc 549																
Pro	Gln	Asn	Asp 135	Gly	Lys	Glu	Leu 140	Cys	Pro	Pro	Gly	Lys	Pro	Thr	Thr 145	
tct gag aag att cac gag aga tct gga aat agg gag gcc caa gaa aag 597																
Ser	Glu	Lys 150	Ile	His	Glu	Arg	Ser 155	Gly	Asn	Arg	Glu	Ala 160	Gln	Glu	Lys	
gaa gag aga cgc gga aca gct cat cgg tgg agc agt cag aac aca cac 645																
Glu	Glu	Arg	Arg	Gly	Thr	Ala 170	His	Arg	Trp	Ser 175	Ser	Gln	Asn	Thr	His	
aac att ggt cga ttc agt ttg tca act tct atg ggt gca gtt cat ggt 693																
Asn	Ile	Gly	Arg	Phe	Ser 185	Leu	Ser	Thr	Ser 190	Met	Gly	Ala	Val	His	Gly 195	
acc ccc aaa aca att aca cac aac agg gac cca aaa ggg ggg aac atg 741																
Thr	Pro	Lys	Thr 200	Ile	Thr	His	Asn	Arg 205	Asp	Pro	Lys	Gly	Gly	Asn	Met 210	
cct gga ccc aca gac tgc gtg aga gaa aac agc tgg tga tttatgaaga 790																
Pro	Gly	Pro	Thr 215	Asp	Cys	Val	Arg	Glu 220	Asn	Ser	Trp					
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Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
20          25          30

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Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
35          40          45

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Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
50          55          60

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Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
65          70          75          80

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Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
85          90          95

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Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
100         105         110

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Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
115         120         125

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Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
130         135         140

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Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Asn Arg Glu Ala
145         150         155         160

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Gln Glu Lys Glu Glu Arg Arg Gly Thr Ala His Arg Trp Ser Ser Gln

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Asn Thr His Asn Ile Gly Arg Phe Ser Leu Ser Thr Ser Met Gly Ala	180	185	190	
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		Met Asn Gly Asp Asp Ala Phe		
		1 5		
gca agg aga ccc acg gtt ggt gct caa ata cca gag aag atc caa aag				162
Ala Arg Arg Pro Thr Val Gly Ala Gln Ile Pro Glu Lys Ile Gln Lys	10	15	20	
gcc ttc gat gat att gcc aaa tac ttc tct aag gaa gag tgg gaa aag				210
Ala Phe Asp Asp Ile Ala Lys Tyr Phe Ser Lys Glu Glu Trp Glu Lys	25	30	35	
atg aaa gcc tcg gag aaa atc ttc tat gtg tat atg aag aga aag tat				258
Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys Arg Lys Tyr	40	45	50	55
gag gct atg act aaa cta ggt ttc aag gcc acc ctc cca cct ttc atg				306
Glu Ala Met Thr Lys Leu Gly Phe Lys Ala Thr Leu Pro Pro Phe Met	60	65	70	
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Cys Asn Lys Arg Ala Glu Asp Phe Gln Gly Asn Asp Leu Asp Asn Asp	75	80	85	
cct aac cgt ggg aat cag gtt gaa cgt cct cag atg act ttc ggc agg				402
Pro Asn Arg Gly Asn Gln Val Glu Arg Pro Gln Met Thr Phe Gly Arg	90	95	100	
ctc cag gga atc tcc ccg aag atc atg ccc aag aag cca gca gag gaa				450

Leu	Gln	Gly	Ile	Ser	Pro	Lys	Ile	Met	Pro	Lys	Lys	Pro	Ala	Glu	Glu		
105						110					115						
gga	aat	gat	tcg	gag	gaa	gtg	cca	gaa	gca	tct	ggc	cca	caa	aat	gat	498	
Gly	Asn	Asp	Ser	Glu	Glu	Val	Pro	Glu	Ala	Ser	Gly	Pro	Gln	Asn	Asp		
120					125					130				135			
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Gly	Lys	Glu	Leu	Cys	Pro	Pro	Gly	Lys	Pro	Thr	Thr	Ser	Glu	Lys	Ile		
				140					145					150			
nnn	nnn	nnn	nnn	nng	acc	caa	aag	ggg	gga	aca	tgc	ctg	gac	cca	cag	594	
Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Gln	Lys	Gly	Gly	Thr	Cys	Leu	Asp	Pro	Gln		
			155					160					165				
act	gcg	tga	gagaaaacag	ctggtgattt	atgaagagat	cagcgaccct										643	
Thr	Ala																
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caagtgaaag	caagtgttca	caacagtga	aagttgagcg	tcgtttttct	tagtgtgaca											823	
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<220>
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 <222> (153)..(153)
 <223> The 'Xaa' at location 153 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

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<221> misc_feature
 <222> (154)..(154)
 <223> The 'Xaa' at location 154 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>
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 <222> (155)..(155)
 <223> The 'Xaa' at location 155 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, Cys, or Phe.

<220>
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 <222> (156)..(156)
 <223> The 'Xaa' at location 156 stands for Lys, Arg, Thr, Met, Glu, Gly, Ala, Val, Gln, Pro, Leu, Trp, or Ser.

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Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
 20 25 30

Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
 35 40 45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
 50 55 60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
 65 70 75 80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
 85 90 95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
 100 105 110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
 115 120 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
 130 135 140

Pro Thr Thr Ser Glu Lys Ile Xaa Xaa Xaa Xaa Xaa Thr Gln Lys Gly
 145 150 155 160

Gly Thr Cys Leu Asp Pro Gln Thr Ala

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Ile Pro Glu Lys Ile Gln
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Ala Lys Tyr Phe Ser Lys
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<210> 9
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 <212> PRT
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Phe Asp Asp Ile Ala Lys Tyr Phe Ser Lys Glu Glu Trp Glu Lys Met
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Lys Ala Ser Glu Lys Ile
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<210> 10
 <211> 22
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 <213> Homo sapiens

<400> 10

Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys
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Arg Lys Tyr Glu Ala Met
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<210> 11
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Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
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Ala Thr Leu Pro Pro Phe
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<210> 12
<211> 22
<212> PRT
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Glu Asp Phe Gln Gly Asn
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<210> 13
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Arg Leu Gln

<210> 15

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Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
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Pro Lys Lys Pro Ala Glu
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Glu Val Pro Glu Ala Ser
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Asn Asp Ser Glu Glu Val Pro Glu Ala Ser Gly Pro Gln Asn Asp Gly
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Lys Glu Leu Cys Pro Pro
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Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys Pro Thr Thr Ser
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Glu Lys Ile His Glu Arg
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Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
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Glu His Ala Trp Thr His
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Pro Lys Arg Gly Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys
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Gln Leu Val Ile Tyr Glu
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<213> Homo sapiens

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Arg Glu Arg Lys Gln Leu Val Ile Tyr Glu Glu Ile Ser Asp Pro Glu
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Glu Asp Asp Glu
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Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr Val Tyr Met Lys Arg Lys
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Tyr Glu Ala Met
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Ala Met

<210> 24

<211> 16

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1 5 10

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<211> 12

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<213> Homo sapiens

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1 5 10

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Arg Lys Tyr Glu
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Arg Lys

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1 5 10

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<400> 37

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<210> 38
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Lys Ile Val Tyr Val Tyr Met Lys Leu Asn Tyr Glu Val Met
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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Phe	Gly	Arg	Leu	Gln	Gly	Ile	Ser	Pro	Lys	Ile	Met	Pro	Lys	Lys
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<212> PRT

<213> Homo sapiens

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Tyr	Ala	Phe	Arg	Ala	Ser	Ala	Lys	Ala
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<213> Homo sapiens

<400> 51

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48